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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: LAURE ZARA Examiner #: 77518 Date: 7/11/05
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 096735363
Location (Bldg/Room#): 2D28 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER DISK ME

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Nonrepetitively useful synthetic design
Inventors (please provide full names): Phillips et al.

Earliest Priority Date: 12/12/00

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search Seq ID Nos

8, 10, 25, 42, 43 + 45

For Seq 8, please limit to size of 3 NTS.

For Seq 10, please limit to size of 6 NTS.

For Seq 42, please limit to size of 6 NTS.

For Seq 43, please limit size to 6 NTS.

For Seq 45, please limit size to 6 NTS.

Please Search Interference + regular
date lines. Thanks.

STAFF USE ONLY

Searcher: _____	Type of Search	Vendors and cost where applicable
Searcher Phone #: _____	____ NA Sequence (#)	____ STN ____ Dialog
Searcher Location: _____	____ AA Sequence (#)	____ Questel/Orbit ____ Lexis/Nexis
Date Searcher Picked Up: _____	____ Structure (#)	____ Westlaw ____ WWW/Internet
	____ Bibliographic	____ In-house sequence systems
Date Completed: _____	____ Litigation	____ Commercial ____ Oligomer ____ Score/Length
Searcher Prep & Review Time: _____	____ Fulltext	____ Interference ____ SPDI ____ Encode/Transl
Online Time: _____	____ Other	____ Other (specify)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 23:06:00 ; Search time 1253.4 Seconds
(without alignments)
23.814 Million cell updates/sec

Title: US-09-735-363A-25
Perfect score: 6
Sequence: 1 gsgtgg 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16353451.seqs, 2487343176 residues

Total number of hits satisfying chosen parameters: 2336

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Pending Patents NA New:
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:
2: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:
3: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:
4: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:
5: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:
6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:
7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:
8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:
9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:
10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:
11: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:
12: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:
13: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:
14: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:
15: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:
16: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:
17: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID

Thu Jul 21 10:31:18 2005

us-09-735-363a-42.szlm6.rnpn

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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:36:35 ; Search time 1796 Seconds
(without alignments)
136.380 Million cell updates/sec

Title: US-09-735-363A-42
Perfect score: 6
Sequence: 1 ggaagg 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 13936

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Pending Patents_NA_Main*

OM_nucleic - nucleic search, using sw model

Run on:	July 20, 2005, 23:06:00	Search time 1253.4 Seconds (without alignments)
		23.814 Million cell updates/sec

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 2336

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100

```

Database : Pending Patents NA New.*
1: /cgm2_6/ptodata/1/pna/PCT_NEW COMB.seq:*
2: /cgm2_6/ptodata/1/pna/PCT_NEW COMB.seq:2:*
3: /cgm2_6/ptodata/1/pna/US06 NEW COMB.seq:*
4: /cgm2_6/ptodata/1/pna/US07 NEW COMB.seq:*
5: /cgm2_6/ptodata/1/pna/US08 NEW COMB.seq:*
6: /cgm2_6/ptodata/1/pna/US09 NEW COMB.seq:*
7: /cgm2_6/ptodata/1/pna/US10 NEW COMB.seq:*
8: /cgm2_6/ptodata/1/pna/US10 NEW COMB.seq:2:*
9: /cgm2_6/ptodata/1/pna/US10 NEW COMB.seq:3:*
10: /cgm2_6/ptodata/1/pna/US10 NEW COMB.seq:4:*
11: /cgm2_6/ptodata/1/pna/US10 NEW COMB.seq:5:*
12: /cgm2_6/ptodata/1/pna/US10 NEW COMB.seq:6:*
13: /cgm2_6/ptodata/1/pna/US11 NEW COMB.seq:*
14: /cgm2_6/ptodata/1/pna/US11 NEW COMB.seq:2:*
15: /cgm2_6/ptodata/1/pna/US11 NEW COMB.seq:3:*
16: /cgm2_6/ptodata/1/pna/US11 NEW COMB.seq:4:*
17: /cgm2_6/ptodata/1/pna/US16 NEW COMB.seq:*

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100	100	100	1	...

Thu Jul 21 10:31:20 2005

us-09-735-363a-43.szlm6.rnppm

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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:36:35 ; Search time 1796 Seconds
(without alignments)
136.380 Million cell updates/sec

Title: US-09-735-363A-43

Perfect score: 6

Sequence: 1 ggccgg 6

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4554873 seqs, 2041521753 residues

Total number of hits satisfying chosen parameters: 13936

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Pending Patents_NA_Main*

Thu Jul 21 10:31:22 2005

us-09-735-363a-45.szlm6.rnppm

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:36:35 ; Search time 1796 Seconds
(without alignments)
136.380 Million cell updates/sec

Title: US-09-735-363A-45

Perfect score: 6

Sequence: 1 gggagg 6

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 13936

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Pending Patents NA Main:*

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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 23:06:00 ; Search time 1253.4 Seconds
(without alignments)
23.814 Million cell updates/sec

Title: US-09-735-363A-43
Perfect score: 6
Sequence: 1 ggcgg 6

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16353451 seqs, 2487343176 residues

Total number of hits satisfying chosen parameters: 2336

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Pending Patents NA New:
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:
2: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:
3: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:
4: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:
5: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:
6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:
7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:
8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:
9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:
10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:
11: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:
12: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:
13: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:
14: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:
15: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:
16: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:
17: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 23:06:00 ; Search time 1253.4 Seconds
(without alignments)
23.814 Million cell updates/sec

Title: US-09-735-363A-45
Perfect score: 6
Sequence: 1 gggagg 6

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16353451 seqs, 2487343176 residues

Total number of hits satisfying chosen parameters: 2336

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Pending Patents NA New.*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
2: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq2.*
3: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2.*
9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq3.*
10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq4.*
11: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq5.*
12: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq6.*
13: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq.*
14: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq2.*
15: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq3.*
16: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq4.*
17: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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Thu Jul 21 10:31:15 2005

us-09-735-363a-10.szlm6.rnppm

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:36:35 ; Search time 1796 Seconds
(without alignments)
136.380 Million cell updates/sec

Title: US-09-735-363A-10

Perfect score: 6

Sequence: 1 gtgtgt 6

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 13936

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Pending Patents_NA_Main:*

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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 23:06:00 ; Search time 1253.4 Seconds
(without alignments)
23.814 Million cell updates/sec

Title: US-09-735-363A-10
Perfect score: 6
Sequence: 1 ggtgt 6

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16353451 seqs, 2487343176 residues

Total number of hits satisfying chosen parameters: 2336

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Pending Patents NA New:
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:
2: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:
3: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:
4: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:
5: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:
6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:
7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:
8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:
9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:
10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:
11: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:
12: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:
13: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:
14: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:
15: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:
16: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:
17: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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Thu Jul 21 10:31:23 2005

us-09-735-363a-8.szlm3.rnppm

GenCore version 5.1.6
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OM nucleic acid nucleic search, using sw model

Run on: July 20, 2005, 20:42:19 ; Search time 2266 Seconds
(without alignments)
54.046 Million cell updates/sec

Title: US-09-735-363A-8
Perfect score: 3
Sequence: 1 gtg 3

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 2500

Minimum DB seq length: 0
Maximum DB seq length: 3

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Pending Patents_NA_Main:*

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 20:46:47 ; Search time 644 Seconds
(without alignments)
23.168 Million cell updates/sec

Title: US-09-735-363A-8
Perfect score: 3
Sequence: 1 gtc 3

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16351682 seqs, 2486654067 residues

Total number of hits satisfying chosen parameters: 132

Minimum DB seq length: 0
Maximum DB seq length: 3

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

- Pending Patents NA New:*
- 1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
 - 2: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq2:*
 - 3: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
 - 4: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
 - 5: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
 - 6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
 - 7: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
 - 8: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq2:*
 - 9: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq3:*
 - 10: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq4:*
 - 11: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq5:*
 - 12: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq6:*
 - 13: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:*
 - 14: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq2:*
 - 15: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq3:*
 - 16: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq4:*
 - 17: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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Thu Jul 21 10:31:17 2005

us-09-735-363a-25.szlm6.rnrm

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:36:35 ; Search time 1796 Seconds
(without alignments)
136.380 Million cell updates/sec

Title: US-09-735-363A-25

Perfect score: 6

Sequence: 1 ggggtgg 6

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 2041521753 residues

Total number of hits satisfying chosen parameters: 13936

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Pending_Patents_NA_Main.*